

Appendix II

Alignment of instant SEQ ID NO: 1 (nucleotides 770-1310) with SEQ ID NO: 27 (plasmid pMG) of Perkins et al

>icl1|61939_S1D_27
Length=5627

Sort alignments for thi
E value Score Pos.
Query start position

Score = 765 bits (414), Expect = 0.0
Identities = 414/414 (100%), Gaps = 0/414 (0%)
Strand=Plus/Plus

Query	770	GCCAAAGAGTGAACGTAAGTACCGCCTATAGAGTCATAAGGCCACCCCCCTGGCITCTTAT	829
Sbjct	1879	GCCAAAGAGTGAACGTAAGTACCGCCTATAGAGTCATAAGGCCACCCCCCTGGCITCTTAT	1938
Query	830	GCATGCTATACTGTTTGGCTTGGGGTCTATACACCCCCGGCTCCTCATGTTATAGGTG	889
Sbjct	1939	GCATGCTATACTGTTTGGCTTGGGGTCTATACACCCCCGGCTCCTCATGTTATAGGTG	1998
Query	890	ATGGTATAAGCTTACGCTATAGGTGTGGGTTATTGACCATTATTGACCACTCCCCTATTGG	949
Sbjct	1999	ATGGTATAAGCTTACGCTATAGGTGTGGGTTATTGACCACTCCCCTATTGG	2058
Query	950	TGACCGATACTTCCATTACTAATCCATAACATGGCTTTGCCACAACTCTCTTATTGG	1009
Sbjct	2059	TGACCGATACTTCCATTACTAATCCATAACATGGCTTTGCCACAACTCTCTTATTGG	2118
Query	1010	CTATATGCCAATACACTGTCTTCAAGAGACTGACACGGACTCTGTATTTCACAGGATGG	1069
Sbjct	2119	CTATATGCCAATACACTGTCTTCAAGAGACTGACACGGACTCTGTATTTCACAGGATGG	2178
Query	1070	GGTCTCATTIATTATTACAAATTACACATAACACACCACCGTCCCCAGTGCCCCAGT	1129
Sbjct	2179	GGTCTCATTIATTATTACAAATTACACATAACACACCACCGTCCCCAGTGCCCCAGT	2238
Query	1130	TTTTATTAAACATAACGTGGGATCTCCACGCGAATCTCGGGTACGTGTCCCGGA	1183
Sbjct	2239	TTTTATTAAACATAACGTGGGATCTCCACGCGAATCTCGGGTACGTGTCCCGGA	2292

Score = 215 bits (116), Expect = 4e-59
Identities = 116/116 (100%), Gaps = 0/116 (0%)
Strand=Plus/Plus

Query	1183	AACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGGCCACCAAGACA	1242
Sbjct	2607	AACGGTGGAGGGCAGTGTAGTCTGAGCAGTACTCGTTGCTGCCGCGCGGCCACCAAGACA	2666
Query	1243	TAATAGCTGACAGACTAACAGAGACTGTTCTTCCATGGGTCTTCTGAGTCACC	1298
Sbjct	2667	TAATAGCTGACAGACTAACAGAGACTGTTCTTCCATGGGTCTTCTGAGTCACC	2722